

SCORE Search Results Details for Application 10762596 and Search Result us-10-762-596-2.rag.

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GenCore version 5.1.9
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OM protein - protein search, using sw model

```
Run on:      July 25, 2006, 21:29:39 ; Search time 136.5 Seconds
              (without alignments)
              2502.129 Million cell updates/sec
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Title:          US-10-762-596-2
Perfect score: 3815
Sequence:      1 MHSWRWAAAAAAFEKRRHSA.....RKKLQEEIVNSVKGCGNCSC 747
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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7:  geneseqp2003bs:*
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9:  geneseqp2005s:*
10: geneseqp2006s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	3815	100.0	747	8	ADT89439	Adt89439 Human wil
2	3815	100.0	747	9	ADY58462	Ady58462 Human ATP
3	3812	99.9	747	8	ADT89441	Adt89441 Human I39
4	3812	99.9	747	9	ADY58464	Ady58464 Human ATP
5	3812	99.9	752	9	ADY70299	Ady70299 Human bet
6	3806	99.8	747	2	AAW89585	Aaw89585 Human ATP
7	3806	99.8	747	3	AAB13355	Aab13355 Human ATP
8	3712	97.3	752	2	AAV14068	Aay14068 Human ABC
9	3712	97.3	752	5	ABP52103	Abp52103 Homo sapi
10	3632.5	95.2	722	4	AAB92941	Aab92941 Human pro
11	1849	48.5	606	4	ABB57811	Abb57811 Drosophil
12	1849	48.5	606	4	ABB57812	Abb57812 Drosophil
13	1519.5	39.8	690	8	ADN19274	Adn19274 Bacterial
14	1519.5	39.8	690	8	ADT89443	Adt89443 S. cerevi
15	1519.5	39.8	690	9	ADY58466	Ady58466 Yeast mit
16	1466.5	38.4	526	8	ADN21203	Adn21203 Bacterial
17	1396.5	36.6	627	8	ADS23282	Ads23282 Bacterial
18	1376.5	36.1	583	8	ADS25385	Ads25385 Bacterial
19	1374.5	36.0	602	8	ADS25717	Ads25717 Bacterial
20	1327.5	34.8	554	8	ADS24232	Ads24232 Bacterial
21	1297.5	34.0	525	8	ADN26031	Adn26031 Bacterial
22	1274	33.4	495	8	ADN22255	Adn22255 Bacterial
23	1274	33.4	495	8	ADN25013	Adn25013 Bacterial
24	1260.5	33.0	717	8	ADN25117	Adn25117 Bacterial
25	1250	32.8	796	8	ADJ27172	Adj27172 Human TRI
26	1243.5	32.6	490	8	ADS43323	Ads43323 Bacterial
27	1240	32.5	766	6	ADA55337	Ada55337 Human pro
28	1240	32.5	840	8	ADR46659	Adr46659 Cancer-as
29	1240	32.5	842	4	AAU09965	Aau09965 Human ABC
30	1240	32.5	842	5	ABP52102	Abp52102 Homo sapi
31	1240	32.5	842	5	AAE16764	Aae16764 Human tra
32	1240	32.5	842	7	ADE55514	Ade55514 Human Pro
33	1240	32.5	842	7	ADN39963	Adn39963 Cancer/an
34	1231.5	32.3	843	4	AAU00010	Aau00010 Human ABC
35	1228.5	32.2	481	8	ADS22696	Ads22696 Bacterial
36	1228.5	32.2	481	8	ADS26195	Ads26195 Bacterial
37	1225.5	32.1	485	8	ADS42298	Ads42298 Bacterial
38	1218.5	31.9	843	4	AAU00011	Aau00011 Human ABC
39	1204.5	31.6	475	2	AAV08961	Aay08961 A. gossyp
40	1187.5	31.1	927	8	ADR98871	Adr98871 Lung spec
41	1184	31.0	574	3	AAV54454	Aay54454 Amino aci
42	1184	31.0	866	4	ABB71210	Abb71210 Drosophil
43	1176.5	30.8	937	8	ADR98873	Adr98873 Lung spec
44	1175	30.8	571	4	AAM39313	Aam39313 Human pol
45	1150.5	30.2	591	4	AAM41099	Aam41099 Human pol

ALIGNMENTS

RESULT 1

ADT89439

ID ADT89439 standard; protein; 747 AA.

XX

AC ADT89439;

XX

DT 30-DEC-2004 (first entry)

SCORE Search Results Details for Application 10762596 and Search Result us-10-762-596-2.r

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OM protein - protein search, using sw model

Run on: July 25, 2006, 21:41:09 ; Search time 36.5 Seconds
(without alignments)
1791.380 Million cell updates/sec

Title: US-10-762-596-2
Perfect score: 3815
Sequence: 1 MHSWRWAAAAAAFEKRRHSA.....RKKLQEEIVNSVKGCGNCSC 747

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
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7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	3815	100.0	747	US-09-422-840B-2	Sequence 2, Appli
2	3812	99.9	747	US-09-422-840B-4	Sequence 4, Appli

3	3806	99.8	747	1	US-08-895-522-1	Sequence 1, Appli
4	3806	99.8	747	2	US-09-195-391-1	Sequence 1, Appli
5	3339	87.5	694	1	US-08-895-522-3	Sequence 3, Appli
6	3339	87.5	694	2	US-09-195-391-3	Sequence 3, Appli
7	1519.5	39.8	690	2	US-09-422-840B-6	Sequence 6, Appli
8	1519.5	39.8	694	1	US-08-895-522-4	Sequence 4, Appli
9	1519.5	39.8	694	2	US-09-195-391-4	Sequence 4, Appli
10	1240	32.5	766	2	US-10-094-749-2905	Sequence 2905, Ap
11	1204.5	31.6	475	2	US-09-212-247C-4	Sequence 4, Appli
12	1204.5	31.6	475	2	US-10-076-157-4	Sequence 4, Appli
13	695.5	18.2	582	2	US-09-134-001C-4730	Sequence 4730, Ap
14	685	18.0	621	2	US-09-602-787A-342	Sequence 342, App
15	682	17.9	548	2	US-09-710-279-326	Sequence 326, App
16	676.5	17.7	593	2	US-09-543-681A-5368	Sequence 5368, Ap
17	661.5	17.3	513	2	US-09-902-540-11507	Sequence 11507, A
18	651	17.1	575	2	US-09-328-352-7721	Sequence 7721, Ap
19	647.5	17.0	582	2	US-09-489-039A-12080	Sequence 12080, A
20	641.5	16.8	687	2	US-09-302-626B-173	Sequence 173, App
21	641.5	16.8	707	2	US-08-772-270A-4	Sequence 4, Appli
22	641.5	16.8	707	2	US-09-062-126-4	Sequence 4, Appli
23	640.5	16.8	580	2	US-09-134-001C-5611	Sequence 5611, Ap
24	639	16.7	590	2	US-09-134-000C-4456	Sequence 4456, Ap
25	636.5	16.7	274	2	US-09-248-796A-17624	Sequence 17624, A
26	632.5	16.6	715	2	US-09-543-681A-4943	Sequence 4943, Ap
27	631.5	16.6	715	2	US-09-543-681A-7603	Sequence 7603, Ap
28	629.5	16.5	710	2	US-09-302-626B-28	Sequence 28, Appl
29	629	16.5	710	2	US-09-302-626B-30	Sequence 30, Appl
30	620	16.3	605	2	US-09-252-991A-32874	Sequence 32874, A
31	618.5	16.2	617	2	US-09-328-352-6700	Sequence 6700, Ap
32	618.5	16.2	711	2	US-08-772-270A-12	Sequence 12, Appl
33	617.5	16.2	690	2	US-09-302-626B-171	Sequence 171, App
34	615.5	16.1	598	2	US-09-107-532A-6110	Sequence 6110, Ap
35	611.5	16.0	598	2	US-09-107-532A-7027	Sequence 7027, Ap
36	611.5	16.0	1275	2	US-09-749-340-6	Sequence 6, Appli
37	608.5	16.0	1161	2	US-09-817-762-8	Sequence 8, Appli
38	603.5	15.8	719	2	US-09-583-110-4180	Sequence 4180, Ap
39	603.5	15.8	728	2	US-09-107-433-4330	Sequence 4330, Ap
40	602.5	15.8	1207	2	US-09-817-762-7	Sequence 7, Appli
41	599.5	15.7	620	2	US-09-134-000C-4463	Sequence 4463, Ap
42	596	15.6	603	2	US-09-583-110-4187	Sequence 4187, Ap
43	596	15.6	615	2	US-09-107-433-3098	Sequence 3098, Ap
44	594	15.6	1195	2	US-09-873-409-6	Sequence 6, Appli
45	592	15.5	613	2	US-09-107-532A-6935	Sequence 6935, Ap

ALIGNMENTS

RESULT 1

US-09-422-840B-2

; Sequence 2, Application US/09422840B

; Patent No. 6867017

; GENERAL INFORMATION:

; APPLICANT: Dean, Michael

; APPLICANT: Allikmets, Rando

; APPLICANT: Hutchinson, Amy A.

; TITLE OF INVENTION: ATP-BINDING TRANSPORTER (ABC7) AND METHODS FOR DETECTION OF ANE

; TITLE OF INVENTION: ATAXIA

; FILE REFERENCE: 4239-63609

; CURRENT APPLICATION NUMBER: US/09/422,840B

; CURRENT FILING DATE: 1999-10-21

SCORE Search Results Details for Application 10762596 and Search Result us-10-762-596-2.ra

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OM protein - protein search, using sw model

Run on: July 25, 2006, 21:42:09 ; Search time 123.5 Seconds
(without alignments)
2801.794 Million cell updates/sec

Title: US-10-762-596-2
Perfect score: 3815
Sequence: 1 MHSWRWAAAAAFKKRRHSA.....RKKLQEEIVNSVKGCGNCSC 747

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	3815	100.0	747	4 US-10-762-596-2	Sequence 2, Appli
2	3812	99.9	747	4 US-10-762-596-4	Sequence 4, Appli
3	1849	48.5	606	6 US-11-097-143-225	Sequence 225, App

4	1849	48.5	606	6	US-11-097-143-228	Sequence 228, App
5	1654.5	43.4	677	6	US-11-096-568A-34245	Sequence 34245, A
6	1654.5	43.4	678	6	US-11-096-568A-34244	Sequence 34244, A
7	1612.5	42.3	586	6	US-11-096-568A-34246	Sequence 34246, A
8	1584.5	41.5	846	4	US-10-437-963-170558	Sequence 170558,
9	1519.5	39.8	690	4	US-10-369-493-1927	Sequence 1927, Ap
10	1519.5	39.8	690	4	US-10-762-596-6	Sequence 6, Appli
11	1466.5	38.4	526	4	US-10-369-493-3856	Sequence 3856, Ap
12	1407	36.9	467	4	US-10-424-599-161382	Sequence 161382,
13	1396.5	36.6	627	4	US-10-369-493-12315	Sequence 12315, A
14	1376.5	36.1	583	4	US-10-369-493-14418	Sequence 14418, A
15	1374.5	36.0	602	4	US-10-369-493-14750	Sequence 14750, A
16	1327.5	34.8	554	4	US-10-369-493-13265	Sequence 13265, A
17	1297.5	34.0	525	4	US-10-369-493-8684	Sequence 8684, Ap
18	1274	33.4	495	4	US-10-369-493-4908	Sequence 4908, Ap
19	1274	33.4	495	4	US-10-369-493-7666	Sequence 7666, Ap
20	1260.5	33.0	717	4	US-10-369-493-7770	Sequence 7770, Ap
21	1248	32.7	836	3	US-09-953-688A-7	Sequence 7, Appli
22	1248	32.7	836	5	US-10-878-652-7	Sequence 7, Appli
23	1243.5	32.6	490	4	US-10-369-493-21753	Sequence 21753, A
24	1240	32.5	766	4	US-10-094-749-2905	Sequence 2905, Ap
25	1240	32.5	840	5	US-10-783-528-72	Sequence 72, Appl
26	1240	32.5	842	4	US-10-297-022-1	Sequence 1, Appli
27	1240	32.5	842	4	US-10-295-027-1281	Sequence 1281, Ap
28	1240	32.5	842	4	US-10-220-764-2	Sequence 2, Appli
29	1228.5	32.2	481	4	US-10-369-493-11729	Sequence 11729, A
30	1228.5	32.2	481	4	US-10-369-493-15228	Sequence 15228, A
31	1225.5	32.1	485	4	US-10-369-493-20728	Sequence 20728, A
32	1204.5	31.6	407	4	US-10-425-115-333618	Sequence 333618,
33	1204.5	31.6	475	4	US-10-076-157-4	Sequence 4, Appli
34	1184	31.0	574	3	US-09-953-688A-1	Sequence 1, Appli
35	1184	31.0	574	5	US-10-878-652-1	Sequence 1, Appli
36	1184	31.0	866	6	US-11-097-143-40422	Sequence 40422, A
37	1171.5	30.7	483	4	US-10-425-115-333619	Sequence 333619,
38	1143.5	30.0	482	4	US-10-369-493-10576	Sequence 10576, A
39	1112.5	29.2	477	4	US-10-369-493-17811	Sequence 17811, A
40	1058	27.7	409	4	US-10-369-493-9577	Sequence 9577, Ap
41	1039	27.2	643	4	US-10-369-493-16872	Sequence 16872, A
42	965	25.3	582	4	US-10-369-493-12465	Sequence 12465, A
43	936	24.5	592	4	US-10-369-493-4224	Sequence 4224, Ap
44	932.5	24.4	505	4	US-10-369-493-22763	Sequence 22763, A
45	915	24.0	772	4	US-10-369-493-5898	Sequence 5898, Ap

ALIGNMENTS

RESULT 1

US-10-762-596-2

; Sequence 2, Application US/10762596

; Publication No. US20040203073A1

; GENERAL INFORMATION:

; APPLICANT: Dean, Michael

; APPLICANT: Allikmets, Rando

; APPLICANT: Hutchinson, Amy A.

; TITLE OF INVENTION: ATP-BINDING TRANSPORTER (ABC7) AND METHODS FOR DETECTION OF ANE

; TITLE OF INVENTION: ATAXIA

; FILE REFERENCE: 4239-67289

; CURRENT APPLICATION NUMBER: US/10/762,596

; CURRENT FILING DATE: 2004-01-21

; PRIOR APPLICATION NUMBER: US 09/422,840

SCORE Search Results Details for Application 10762596 and Search Result us-10-762-596-2.rapbn.

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OM protein - protein search, using sw model

```
Run on:      July 25, 2006, 21:43:29 ; Search time 21 Seconds
              (without alignments)
              2051.339 Million cell updates/sec
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```
Title:          US-10-762-596-2
Perfect score: 3815
Sequence:      1 MHSWRWAAAAAAFEKRRHSA.....RKKLQEEIVNSVKGCGNCSC 747
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 208217 seqs, 57668156 residues

Total number of hits satisfying chosen parameters: 208217

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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3:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
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1	1689	44.3	733	6	US-10-449-902-35674	Sequence 35674, A
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3	1654.5	43.4	677	7	US-11-056-355B-111852	Sequence 111852,
4	1654.5	43.4	678	7	US-11-056-355B-100612	Sequence 100612,
5	1654.5	43.4	678	7	US-11-056-355B-111851	Sequence 111851,
6	1617.5	42.4	679	7	US-11-056-355B-81236	Sequence 81236, A
7	1617.5	42.4	680	7	US-11-056-355B-81235	Sequence 81235, A
8	1612.5	42.3	586	7	US-11-056-355B-100614	Sequence 100614,
9	1612.5	42.3	586	7	US-11-056-355B-111853	Sequence 111853,
10	1612	42.3	621	7	US-11-056-355B-81237	Sequence 81237, A
11	1064	27.9	535	6	US-10-449-902-40785	Sequence 40785, A
12	739.5	19.4	281	6	US-10-449-902-55767	Sequence 55767, A
13	699.5	18.3	578	6	US-10-471-571A-1656	Sequence 1656, Ap
14	661.5	17.3	375	6	US-10-449-902-50898	Sequence 50898, A
15	637	16.7	1258	7	US-11-056-355B-85264	Sequence 85264, A
16	637	16.7	1287	7	US-11-056-355B-85263	Sequence 85263, A
17	637	16.7	1298	7	US-11-056-355B-85262	Sequence 85262, A
18	634	16.6	1187	7	US-11-056-355B-73529	Sequence 73529, A
19	634	16.6	1216	7	US-11-056-355B-73528	Sequence 73528, A
20	634	16.6	1227	7	US-11-056-355B-73527	Sequence 73527, A
21	630	16.5	575	6	US-10-471-571A-3150	Sequence 3150, Ap
22	626	16.4	653	6	US-10-449-902-37627	Sequence 37627, A
23	622	16.3	690	6	US-10-449-902-47837	Sequence 47837, A
24	620	16.3	690	6	US-10-449-902-45082	Sequence 45082, A
25	617	16.2	1286	7	US-11-056-355B-99170	Sequence 99170, A
26	617	16.2	1286	7	US-11-056-355B-110409	Sequence 110409,
27	616.5	16.2	1243	7	US-11-056-355B-99171	Sequence 99171, A
28	616.5	16.2	1243	7	US-11-056-355B-110410	Sequence 110410,
29	616	16.1	644	7	US-11-056-355B-18338	Sequence 18338, A
30	616	16.1	648	7	US-11-056-355B-18337	Sequence 18337, A
31	615	16.1	641	6	US-10-449-902-43955	Sequence 43955, A
32	614.5	16.1	1214	7	US-11-056-355B-71658	Sequence 71658, A
33	614.5	16.1	1221	7	US-11-056-355B-71763	Sequence 71763, A
34	614.5	16.1	1222	7	US-11-056-355B-71657	Sequence 71657, A
35	614.5	16.1	1229	7	US-11-056-355B-71762	Sequence 71762, A
36	614.5	16.1	1247	7	US-11-056-355B-71656	Sequence 71656, A
37	614.5	16.1	1254	7	US-11-056-355B-71761	Sequence 71761, A
38	613	16.1	1286	6	US-10-953-349-4545	Sequence 4545, Ap
39	613	16.1	1286	7	US-11-056-355B-28889	Sequence 28889, A
40	613	16.1	1286	7	US-11-056-355B-28970	Sequence 28970, A
41	613	16.1	1286	7	US-11-056-355B-32479	Sequence 32479, A
42	613	16.1	1286	7	US-11-056-355B-32560	Sequence 32560, A
43	612.5	16.1	1243	6	US-10-953-349-4546	Sequence 4546, Ap
44	612.5	16.1	1243	7	US-11-056-355B-28890	Sequence 28890, A
45	612.5	16.1	1243	7	US-11-056-355B-28971	Sequence 28971, A

ALIGNMENTS

RESULT 1

US-10-449-902-35674

; Sequence 35674, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

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OM protein - protein search, using sw model

Run on: July 25, 2006, 21:34:54 ; Search time 29 Seconds
(without alignments)
2478.411 Million cell updates/sec

Title: US-10-762-596-2
Perfect score: 3815
Sequence: 1 MHSWRWAAAAAAFEKRRHSA.....RKKLQEEIVNSVKGCGNCSC 747

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	1654.5	43.4	677	2 T10657	probable ABC-type
2	1617.5	42.4	680	2 T10656	probable ABC-type
3	1541.5	40.4	693	2 T39154	probable ABC trans
4	1519.5	39.8	690	2 S54211	ATM1 protein precu
5	1454.5	38.1	631	2 AH0315	probable ABC trans
6	1446	37.9	609	2 G71731	mitochondrial tran
7	1403	36.8	628	2 AF3438	heavy metal tolera
8	1378	36.1	628	2 AG2707	hypothetical prote

9	1378	36.1	629	2	H97489	mitochondrial tran
10	1248	32.7	836	2	JE0248	ATP-binding casset
11	1039	27.2	643	2	C87412	ABC transporter, H
12	971.5	25.5	830	2	S25198	vacuolar membrane
13	924.5	24.2	1025	2	T18376	multidrug resistan
14	915	24.0	772	2	T26313	hypothetical prote
15	722	18.9	642	2	F84172	ABC transport prot
16	710	18.6	581	2	E83790	ABC transporter (A
17	708	18.6	597	2	AD2074	ATP-binding protei
18	706.5	18.5	593	2	S75352	ABC-type transport
19	699.5	18.3	578	2	A89974	hypothetical prote
20	688	18.0	585	2	H69857	ABC transporter (A
21	687.5	18.0	832	2	B87673	ABC transporter, H
22	678.5	17.8	602	2	A75590	ABC transporter, A
23	675.5	17.7	594	2	S72638	hypothetical ABC e
24	675.5	17.7	604	2	F69802	ABC transporter (A
25	673.5	17.7	546	2	AG1886	ATP-binding protei
26	673.5	17.7	600	2	H98149	ATP-binding transp
27	673.5	17.7	600	2	AD3138	hypothetical prote
28	673.5	17.7	863	2	C90482	ABC transporter, A
29	672.5	17.6	707	1	LEECB	hemolysin secretio
30	671.5	17.6	611	2	AH3540	ABC transporter AT
31	671.5	17.6	707	2	S10057	ABC-type transport
32	670.5	17.6	584	2	E83767	ABC transporter (A
33	667.5	17.5	599	2	AD3017	hypothetical prote
34	667.5	17.5	599	2	D98267	ABC transporter AT
35	665	17.4	600	2	AI2454	ATP-binding protei
36	662	17.4	595	2	T31077	probable ABC-trans
37	662	17.4	650	2	T17482	ABC-type transport
38	655	17.2	708	2	C30169	leukotoxin express
39	654	17.1	582	2	AF0614	probable transport
40	653	17.1	607	2	A95911	hypothetical prote
41	653	17.1	893	2	AH2007	toxin secretion AB
42	651.5	17.1	707	2	A61378	leukotoxin express
43	651	17.1	580	2	C71182	probable ABC trans
44	651	17.1	582	2	E90753	ATP-binding transp
45	651	17.1	582	2	S27998	probable ABC-type

ALIGNMENTS

RESULT 1

T10657

probable ABC-type transport protein T5F17.80 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-Oct-2004

C;Accession: T10657

R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Banc submitted to the Protein Sequence Database, June 1999

A;Reference number: Z16533

A;Accession: T10657

A;Molecule type: DNA

A;Residues: 1-677

A;Cross-references: UNIPROT:Q9M0G8; UNIPARC:UPI00000A7E39; EMBL:AL049917; GSPDB:GN0006

A;Experimental source: cultivar Columbia; BAC clone T5F17

C;Genetics:

A;Gene: ATSP:T5F17.80

A;Map position: 4

A;Introns: 519/3

F;452-646/Domain: ATP-binding cassette homology

SCORE Search Results Details for Application 10762596 and Search Result us-10-762-596-2.rup.

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OM protein - protein search, using sw model

Run on: July 25, 2006, 21:30:09 ; Search time 186.5 Seconds
(without alignments)
3705.022 Million cell updates/sec

Title: US-10-762-596-2
Perfect score: 3815
Sequence: 1 MHSWRWAAAAAAFEKRRHSA.....RKKLQEEIVNSVKGCGNCSC 747

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Match	Query Length	ID	Description
No.			DB		
1	3812	99.9	752 1	ABCB7_HUMAN	O75027 homo sapien
2	3522	92.3	752 1	ABCB7_RAT	Q704e8 rattus norv
3	3511	92.0	752 2	Q3U7S8_MOUSE	Q3u7s8 m bone marr
4	3339	87.5	694 1	ABCB7_MOUSE	Q61102 mus musculu

5	3196.5	83.8	651	2	Q2PFV1_MACFA	Q2pfv1 macaca fasc
6	2570	67.4	644	2	Q4SJU8_TETNG	Q4sju8 tetraodon n
7	1897.5	49.7	594	2	Q7Q5L7_ANOGA	Q7q5l7 anopheles g
8	1879	49.3	743	2	Q9W0C5_DROME	Q9w0c5 drosophila
9	1862.5	48.8	709	2	Q7KVB1_DROME	Q7kvb1 drosophila
10	1849	48.5	606	2	Q7KVA9_DROME	Q7kva9 drosophila
11	1803	47.3	703	2	Q71JP9_CAEEL	Q71jp9 caenorhabdi
12	1797	47.1	715	2	Q61XG8_CAEER	Q61xg8 caenorhabdi
13	1719	45.1	728	2	Q9LVM1_ARATH	Q9lvm1 arabidopsis
14	1707	44.7	728	2	Q9LF78_ARATH	Q9lf78 arabidopsis
15	1687	44.2	733	2	Q658I3_ORYSA	Q658i3 oryza sativ
16	1654.5	43.4	677	2	Q9M0G8_ARATH	Q9m0g8 arabidopsis
17	1654.5	43.4	678	2	Q9FUT3_ARATH	Q9fut3 arabidopsis
18	1628	42.7	727	2	Q4WLN7_ASPFU	Q4wln7 aspergillus
19	1618	42.4	716	2	Q7RX59_NEUCR	Q7rx59 neurospora
20	1617.5	42.4	680	2	Q9M0G9_ARATH	Q9m0g9 arabidopsis
21	1616	42.4	698	2	Q4HVV7_GIBZE	Q4hvv7 gibberella
22	1614	42.3	720	2	Q2ULH4_ASPOR	Q2ulh4 aspergillus
23	1598	41.9	763	2	Q4PH16_USTMA	Q4ph16 ustilago ma
24	1596	41.8	697	2	Q8T9W2_DICDI	Q8t9w2 dictyosteli
25	1554.5	40.7	734	2	Q5KBN9_CRYNE	Q5kbn9 cryptococcu
26	1553.5	40.7	734	2	Q55NA7_CRYNE	Q55na7 cryptococcu
27	1553	40.7	701	2	Q5B1Q2_EMENI	Q5b1q2 aspergillus
28	1551.5	40.7	696	2	Q6BXD7_DEBHA	Q6bxd7 debaryomyce
29	1541.5	40.4	693	1	YD01_SCHPO	O14286 schizosacch
30	1519.5	39.8	690	1	ATM1_YEAST	P40416 saccharomyc
31	1518.5	39.8	720	2	Q6CX96_KLULA	Q6cx96 kluyveromyc
32	1506	39.5	691	2	Q751N2_ASHGO	Q751n2 ashbya goss
33	1503.5	39.4	750	2	Q59R09_CANAL	Q59r09 candida alb
34	1498	39.3	727	2	Q6FIK3_CANGA	Q6fik3 candida gla
35	1469	38.5	605	2	Q7VZK3_BORPE	Q7vzk3 bordetella
36	1458.5	38.2	588	2	Q7WHV3_BORBR	Q7whv3 bordetella
37	1456	38.2	710	2	Q6C6N0_YARLI	Q6c6n0 yarrowia li
38	1455.5	38.2	606	2	Q2YB82_NITMU	Q2yb82 nitrosospir
39	1455	38.1	605	2	Q7W9X4_BORPA	Q7w9x4 bordetella
40	1454.5	38.1	631	2	Q8ZDI0_YERPE	Q8zdi0 yersinia pe
41	1453.5	38.1	596	2	Q8D129_YERPE	Q8d129 yersinia pe
42	1453.5	38.1	596	2	Q66DG4_YERPS	Q66dg4 yersinia ps
43	1447	37.9	592	2	Q68XG3_RICTY	Q68xg3 rickettsia
44	1446	37.9	600	2	Q4UKL9_RICFE	Q4ukl9 rickettsia
45	1446	37.9	609	2	Q9ZDW0_RICPR	Q9zdw0 rickettsia

ALIGNMENTS

RESULT 1

ABCB7_HUMAN

ID ABCB7_HUMAN STANDARD; PRT; 752 AA.
AC O75027; O75345; Q5VWY7; Q5VWY8; Q9BRE1; Q9UND1; Q9UP01;
DT 15-DEC-1998, integrated into UniProtKB/Swiss-Prot.
DT 01-DEC-2000, sequence version 2.
DT 07-MAR-2006, entry version 54.
DE ATP-binding cassette sub-family B member 7, mitochondrial precursor
DE (ATP-binding cassette transporter 7) (ABC transporter 7 protein).
GN Name=ABCB7; Synonyms=ABC7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;

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OM protein - protein search, using sw model

```
Run on:      July 25, 2006, 21:29:39 ; Search time 136.5 Seconds
              (without alignments)
              2502.129 Million cell updates/sec
```

```
Title:          US-10-762-596-4
Perfect score: 3816
Sequence:      1 MHSWRWAAAAAAFEKRRHSA.....RKKLQEEIVNSVKGCGNCSC 747
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      A_Geneseq_8:*
1:  geneseqp1980s:*
2:  geneseqp1990s:*
3:  geneseqp2000s:*
4:  geneseqp2001s:*
5:  geneseqp2002s:*
6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*
9:  geneseqp2005s:*
10: geneseqp2006s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	3816	100.0	747	8	ADT89441	Adt89441 Human I39
2	3816	100.0	747	9	ADY58464	Ady58464 Human ATP
3	3812	99.9	747	8	ADT89439	Adt89439 Human wil
4	3812	99.9	747	9	ADY58462	Ady58462 Human ATP
5	3809	99.8	752	9	ADY70299	Ady70299 Human bet
6	3803	99.7	747	2	AAW89585	Aaw89585 Human ATP
7	3803	99.7	747	3	AAB13355	Aab13355 Human ATP
8	3709	97.2	752	2	AAV14068	Aay14068 Human ABC
9	3709	97.2	752	5	ABP52103	Abp52103 Homo sapi
10	3629.5	95.1	722	4	AAB92941	Aab92941 Human pro
11	1846	48.4	606	4	ABB57811	Abb57811 Drosophil
12	1846	48.4	606	4	ABB57812	Abb57812 Drosophil
13	1517.5	39.8	690	8	ADN19274	Adn19274 Bacterial
14	1517.5	39.8	690	8	ADT89443	Adt89443 S. cerevi
15	1517.5	39.8	690	9	ADY58466	Ady58466 Yeast mit
16	1464.5	38.4	526	8	ADN21203	Adn21203 Bacterial
17	1394.5	36.5	627	8	ADS23282	Ads23282 Bacterial
18	1374.5	36.0	583	8	ADS25385	Ads25385 Bacterial
19	1372.5	36.0	602	8	ADS25717	Ads25717 Bacterial
20	1325.5	34.7	554	8	ADS24232	Ads24232 Bacterial
21	1295.5	33.9	525	8	ADN26031	Adn26031 Bacterial
22	1272	33.3	495	8	ADN22255	Adn22255 Bacterial
23	1272	33.3	495	8	ADN25013	Adn25013 Bacterial
24	1258.5	33.0	717	8	ADN25117	Adn25117 Bacterial
25	1248	32.7	796	8	ADJ27172	Adj27172 Human TRI
26	1241.5	32.5	490	8	ADS43323	Ads43323 Bacterial
27	1238	32.4	766	6	ADA55337	Ada55337 Human pro
28	1238	32.4	840	8	ADR46659	Adr46659 Cancer-as
29	1238	32.4	842	4	AAU09965	Aau09965 Human ABC
30	1238	32.4	842	5	ABP52102	Abp52102 Homo sapi
31	1238	32.4	842	5	AAE16764	Aae16764 Human tra
32	1238	32.4	842	7	ADE55514	Ade55514 Human Pro
33	1238	32.4	842	7	ADN39963	Adn39963 Cancer/an
34	1229.5	32.2	843	4	AAU00010	Aau00010 Human ABC
35	1226.5	32.1	481	8	ADS22696	Ads22696 Bacterial
36	1226.5	32.1	481	8	ADS26195	Ads26195 Bacterial
37	1223.5	32.1	485	8	ADS42298	Ads42298 Bacterial
38	1216.5	31.9	843	4	AAU00011	Aau00011 Human ABC
39	1202.5	31.5	475	2	AAV08961	Aay08961 A. gossyp
40	1185.5	31.1	927	8	ADR98871	Adr98871 Lung spec
41	1182	31.0	574	3	AAV54454	Aay54454 Amino aci
42	1182	31.0	866	4	ABB71210	Abb71210 Drosophil
43	1174.5	30.8	937	8	ADR98873	Adr98873 Lung spec
44	1173	30.7	571	4	AAM39313	Aam39313 Human pol
45	1148.5	30.1	591	4	AAM41099	Aam41099 Human pol

ALIGNMENTS

RESULT 1

ADT89441

ID ADT89441 standard; protein; 747 AA.

XX

AC ADT89441;

XX

DT 30-DEC-2004 (first entry)

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OM protein - protein search, using sw model

Run on: July 25, 2006, 21:41:09 ; Search time 36.5 Seconds
(without alignments)
1791.380 Million cell updates/sec

Title: US-10-762-596-4
Perfect score: 3816
Sequence: 1 MHSWRWAAAAAAFEKRRHSA.....RKKLQEEIVNSVKGCGNCSC 747

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	3816	100.0	747	US-09-422-840B-4	Sequence 4, Appli
2	3812	99.9	747	US-09-422-840B-2	Sequence 2, Appli

3	3803	99.7	747	1	US-08-895-522-1	Sequence 1, Appli
4	3803	99.7	747	2	US-09-195-391-1	Sequence 1, Appli
5	3336	87.4	694	1	US-08-895-522-3	Sequence 3, Appli
6	3336	87.4	694	2	US-09-195-391-3	Sequence 3, Appli
7	1517.5	39.8	690	2	US-09-422-840B-6	Sequence 6, Appli
8	1517.5	39.8	694	1	US-08-895-522-4	Sequence 4, Appli
9	1517.5	39.8	694	2	US-09-195-391-4	Sequence 4, Appli
10	1238	32.4	766	2	US-10-094-749-2905	Sequence 2905, Ap
11	1202.5	31.5	475	2	US-09-212-247C-4	Sequence 4, Appli
12	1202.5	31.5	475	2	US-10-076-157-4	Sequence 4, Appli
13	695.5	18.2	582	2	US-09-134-001C-4730	Sequence 4730, Ap
14	685	18.0	621	2	US-09-602-787A-342	Sequence 342, App
15	682	17.9	548	2	US-09-710-279-326	Sequence 326, App
16	677.5	17.8	593	2	US-09-543-681A-5368	Sequence 5368, Ap
17	662.5	17.4	513	2	US-09-902-540-11507	Sequence 11507, A
18	654	17.1	575	2	US-09-328-352-7721	Sequence 7721, Ap
19	648.5	17.0	582	2	US-09-489-039A-12080	Sequence 12080, A
20	639.5	16.8	687	2	US-09-302-626B-173	Sequence 173, App
21	639.5	16.8	707	2	US-08-772-270A-4	Sequence 4, Appli
22	639.5	16.8	707	2	US-09-062-126-4	Sequence 4, Appli
23	637.5	16.7	580	2	US-09-134-001C-5611	Sequence 5611, Ap
24	637	16.7	590	2	US-09-134-000C-4456	Sequence 4456, Ap
25	636.5	16.7	274	2	US-09-248-796A-17624	Sequence 17624, A
26	629.5	16.5	715	2	US-09-543-681A-4943	Sequence 4943, Ap
27	629.5	16.5	715	2	US-09-543-681A-7603	Sequence 7603, Ap
28	627.5	16.4	710	2	US-09-302-626B-28	Sequence 28, Appl
29	627	16.4	710	2	US-09-302-626B-30	Sequence 30, Appl
30	621	16.3	605	2	US-09-252-991A-32874	Sequence 32874, A
31	616.5	16.2	617	2	US-09-328-352-6700	Sequence 6700, Ap
32	616.5	16.2	711	2	US-08-772-270A-12	Sequence 12, Appl
33	615.5	16.1	598	2	US-09-107-532A-6110	Sequence 6110, Ap
34	615.5	16.1	690	2	US-09-302-626B-171	Sequence 171, App
35	611.5	16.0	1275	2	US-09-749-340-6	Sequence 6, Appli
36	609.5	16.0	598	2	US-09-107-532A-7027	Sequence 7027, Ap
37	608.5	15.9	1161	2	US-09-817-762-8	Sequence 8, Appli
38	603.5	15.8	719	2	US-09-583-110-4180	Sequence 4180, Ap
39	603.5	15.8	728	2	US-09-107-433-4330	Sequence 4330, Ap
40	602.5	15.8	1207	2	US-09-817-762-7	Sequence 7, Appli
41	600	15.7	603	2	US-09-583-110-4187	Sequence 4187, Ap
42	600	15.7	615	2	US-09-107-433-3098	Sequence 3098, Ap
43	599.5	15.7	620	2	US-09-134-000C-4463	Sequence 4463, Ap
44	594	15.6	1195	2	US-09-873-409-6	Sequence 6, Appli
45	591.5	15.5	608	2	US-09-107-532A-5702	Sequence 5702, Ap

ALIGNMENTS

RESULT 1

US-09-422-840B-4

; Sequence 4, Application US/09422840B

; Patent No. 6867017

; GENERAL INFORMATION:

; APPLICANT: Dean, Michael

; APPLICANT: Allikmets, Rando

; APPLICANT: Hutchinson, Amy A.

; TITLE OF INVENTION: ATP-BINDING TRANSPORTER (ABC7) AND METHODS FOR DETECTION OF ANE

; TITLE OF INVENTION: ATAXIA

; FILE REFERENCE: 4239-63609

; CURRENT APPLICATION NUMBER: US/09/422,840B

; CURRENT FILING DATE: 1999-10-21

SCORE Search Results Details for Application 10762596 and Search Result us-10-762-596-4.ra

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OM protein - protein search, using sw model

Run on: July 25, 2006, 21:42:09 ; Search time 123.5 Seconds
(without alignments)
2801.794 Million cell updates/sec

Title: US-10-762-596-4
Perfect score: 3816
Sequence: 1 MHSWRWAAAAAAFEKRRHSA.....RKKLQEEIVNSVKGCGNCSC 747

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3816	100.0	747	US-10-762-596-4	Sequence 4, Appli
2	3812	99.9	747	US-10-762-596-2	Sequence 2, Appli
3	1846	48.4	606	US-11-097-143-225	Sequence 225, App

4	1846	48.4	606	6	US-11-097-143-228	Sequence 228, App
5	1651.5	43.3	677	6	US-11-096-568A-34245	Sequence 34245, A
6	1651.5	43.3	678	6	US-11-096-568A-34244	Sequence 34244, A
7	1609.5	42.2	586	6	US-11-096-568A-34246	Sequence 34246, A
8	1582.5	41.5	846	4	US-10-437-963-170558	Sequence 170558,
9	1517.5	39.8	690	4	US-10-369-493-1927	Sequence 1927, Ap
10	1517.5	39.8	690	4	US-10-762-596-6	Sequence 6, Appli
11	1464.5	38.4	526	4	US-10-369-493-3856	Sequence 3856, Ap
12	1404	36.8	467	4	US-10-424-599-161382	Sequence 161382,
13	1394.5	36.5	627	4	US-10-369-493-12315	Sequence 12315, A
14	1374.5	36.0	583	4	US-10-369-493-14418	Sequence 14418, A
15	1372.5	36.0	602	4	US-10-369-493-14750	Sequence 14750, A
16	1325.5	34.7	554	4	US-10-369-493-13265	Sequence 13265, A
17	1295.5	33.9	525	4	US-10-369-493-8684	Sequence 8684, Ap
18	1272	33.3	495	4	US-10-369-493-4908	Sequence 4908, Ap
19	1272	33.3	495	4	US-10-369-493-7666	Sequence 7666, Ap
20	1258.5	33.0	717	4	US-10-369-493-7770	Sequence 7770, Ap
21	1246	32.7	836	3	US-09-953-688A-7	Sequence 7, Appli
22	1246	32.7	836	5	US-10-878-652-7	Sequence 7, Appli
23	1241.5	32.5	490	4	US-10-369-493-21753	Sequence 21753, A
24	1238	32.4	766	4	US-10-094-749-2905	Sequence 2905, Ap
25	1238	32.4	840	5	US-10-783-528-72	Sequence 72, Appl
26	1238	32.4	842	4	US-10-297-022-1	Sequence 1, Appli
27	1238	32.4	842	4	US-10-295-027-1281	Sequence 1281, Ap
28	1238	32.4	842	4	US-10-220-764-2	Sequence 2, Appli
29	1226.5	32.1	481	4	US-10-369-493-11729	Sequence 11729, A
30	1226.5	32.1	481	4	US-10-369-493-15228	Sequence 15228, A
31	1223.5	32.1	485	4	US-10-369-493-20728	Sequence 20728, A
32	1202.5	31.5	475	4	US-10-076-157-4	Sequence 4, Appli
33	1201.5	31.5	407	4	US-10-425-115-333618	Sequence 333618,
34	1182	31.0	574	3	US-09-953-688A-1	Sequence 1, Appli
35	1182	31.0	574	5	US-10-878-652-1	Sequence 1, Appli
36	1182	31.0	866	6	US-11-097-143-40422	Sequence 40422, A
37	1168.5	30.6	483	4	US-10-425-115-333619	Sequence 333619,
38	1145.5	30.0	482	4	US-10-369-493-10576	Sequence 10576, A
39	1114.5	29.2	477	4	US-10-369-493-17811	Sequence 17811, A
40	1056	27.7	409	4	US-10-369-493-9577	Sequence 9577, Ap
41	1039	27.2	643	4	US-10-369-493-16872	Sequence 16872, A
42	963	25.2	582	4	US-10-369-493-12465	Sequence 12465, A
43	934	24.5	592	4	US-10-369-493-4224	Sequence 4224, Ap
44	930.5	24.4	505	4	US-10-369-493-22763	Sequence 22763, A
45	912	23.9	772	4	US-10-369-493-5898	Sequence 5898, Ap

ALIGNMENTS

RESULT 1

US-10-762-596-4

; Sequence 4, Application US/10762596

; Publication No. US20040203073A1

; GENERAL INFORMATION:

; APPLICANT: Dean, Michael

; APPLICANT: Allikmets, Rando

; APPLICANT: Hutchinson, Amy A.

; TITLE OF INVENTION: ATP-BINDING TRANSPORTER (ABC7) AND METHODS FOR DETECTION OF ANE

; TITLE OF INVENTION: ATAXIA

; FILE REFERENCE: 4239-67289

; CURRENT APPLICATION NUMBER: US/10/762,596

; CURRENT FILING DATE: 2004-01-21

; PRIOR APPLICATION NUMBER: US 09/422,840

SCORE Search Results Details for Application 10762596 and Search Result us-10-762-596-4.rapbn.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

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start

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OM protein - protein search, using sw model

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Run on:      July 25, 2006, 21:43:29 ; Search time 21 Seconds
              (without alignments)
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Perfect score: 3816
Sequence:      1 MHSWRWAAAAAAFEKRRHSA.....RKKLOEEIVNSVKGCGNCSC 747
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 208217 seqs, 57668156 residues

Total number of hits satisfying chosen parameters: 208217

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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8:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1687	44.2	733	6	US-10-449-902-35674	Sequence 35674, A
2	1651.5	43.3	677	7	US-11-056-355B-100613	Sequence 100613,
3	1651.5	43.3	677	7	US-11-056-355B-111852	Sequence 111852,
4	1651.5	43.3	678	7	US-11-056-355B-100612	Sequence 100612,
5	1651.5	43.3	678	7	US-11-056-355B-111851	Sequence 111851,
6	1614.5	42.3	679	7	US-11-056-355B-81236	Sequence 81236, A
7	1614.5	42.3	680	7	US-11-056-355B-81235	Sequence 81235, A
8	1609.5	42.2	586	7	US-11-056-355B-100614	Sequence 100614,
9	1609.5	42.2	586	7	US-11-056-355B-111853	Sequence 111853,
10	1609	42.2	621	7	US-11-056-355B-81237	Sequence 81237, A
11	1062	27.8	535	6	US-10-449-902-40785	Sequence 40785, A
12	739.5	19.4	281	6	US-10-449-902-55767	Sequence 55767, A
13	699.5	18.3	578	6	US-10-471-571A-1656	Sequence 1656, Ap
14	661.5	17.3	375	6	US-10-449-902-50898	Sequence 50898, A
15	637	16.7	1258	7	US-11-056-355B-85264	Sequence 85264, A
16	637	16.7	1287	7	US-11-056-355B-85263	Sequence 85263, A
17	637	16.7	1298	7	US-11-056-355B-85262	Sequence 85262, A
18	634	16.6	1187	7	US-11-056-355B-73529	Sequence 73529, A
19	634	16.6	1216	7	US-11-056-355B-73528	Sequence 73528, A
20	634	16.6	1227	7	US-11-056-355B-73527	Sequence 73527, A
21	627	16.4	575	6	US-10-471-571A-3150	Sequence 3150, Ap
22	626	16.4	653	6	US-10-449-902-37627	Sequence 37627, A
23	620	16.2	690	6	US-10-449-902-47837	Sequence 47837, A
24	618	16.2	690	6	US-10-449-902-45082	Sequence 45082, A
25	617	16.2	1286	7	US-11-056-355B-99170	Sequence 99170, A
26	617	16.2	1286	7	US-11-056-355B-110409	Sequence 110409,
27	616.5	16.2	1243	7	US-11-056-355B-99171	Sequence 99171, A
28	616.5	16.2	1243	7	US-11-056-355B-110410	Sequence 110410,
29	616	16.1	644	7	US-11-056-355B-18338	Sequence 18338, A
30	616	16.1	648	7	US-11-056-355B-18337	Sequence 18337, A
31	615	16.1	641	6	US-10-449-902-43955	Sequence 43955, A
32	614.5	16.1	1214	7	US-11-056-355B-71658	Sequence 71658, A
33	614.5	16.1	1221	7	US-11-056-355B-71763	Sequence 71763, A
34	614.5	16.1	1222	7	US-11-056-355B-71657	Sequence 71657, A
35	614.5	16.1	1229	7	US-11-056-355B-71762	Sequence 71762, A
36	614.5	16.1	1247	7	US-11-056-355B-71656	Sequence 71656, A
37	614.5	16.1	1254	7	US-11-056-355B-71761	Sequence 71761, A
38	613	16.1	1286	6	US-10-953-349-4545	Sequence 4545, Ap
39	613	16.1	1286	7	US-11-056-355B-28889	Sequence 28889, A
40	613	16.1	1286	7	US-11-056-355B-28970	Sequence 28970, A
41	613	16.1	1286	7	US-11-056-355B-32479	Sequence 32479, A
42	613	16.1	1286	7	US-11-056-355B-32560	Sequence 32560, A
43	612.5	16.1	1243	6	US-10-953-349-4546	Sequence 4546, Ap
44	612.5	16.1	1243	7	US-11-056-355B-28890	Sequence 28890, A
45	612.5	16.1	1243	7	US-11-056-355B-28971	Sequence 28971, A

ALIGNMENTS

RESULT 1

US-10-449-902-35674

; Sequence 35674, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

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OM protein - protein search, using sw model

Run on: July 25, 2006, 21:34:54 ; Search time 29 Seconds
(without alignments)
2478.411 Million cell updates/sec

Title: US-10-762-596-4
Perfect score: 3816
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 283416

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
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2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1651.5	43.3	677	2 T10657	probable ABC-type
2	1614.5	42.3	680	2 T10656	probable ABC-type
3	1538.5	40.3	693	2 T39154	probable ABC trans
4	1517.5	39.8	690	2 S54211	ATM1 protein precu
5	1451.5	38.0	631	2 AH0315	probable ABC trans
6	1443	37.8	609	2 G71731	mitochondrial tran
7	1401	36.7	628	2 AF3438	heavy metal tolera
8	1376	36.1	628	2 AG2707	hypothetical prote

9	1376	36.1	629	2	H97489	mitochondrial tran
10	1246	32.7	836	2	JE0248	ATP-binding casset
11	1039	27.2	643	2	C87412	ABC transporter, H
12	969.5	25.4	830	2	S25198	vacuolar membrane
13	925.5	24.3	1025	2	T18376	multidrug resistan
14	912	23.9	772	2	T26313	hypothetical prote
15	722	18.9	642	2	F84172	ABC transport prot
16	708	18.6	581	2	E83790	ABC transporter (A
17	708	18.6	597	2	AD2074	ATP-binding protei
18	706.5	18.5	593	2	S75352	ABC-type transport
19	699.5	18.3	578	2	A89974	hypothetical prote
20	689.5	18.1	832	2	B87673	ABC transporter, H
21	686	18.0	585	2	H69857	ABC transporter (A
22	676.5	17.7	602	2	A75590	ABC transporter, A
23	675.5	17.7	594	2	S72638	hypothetical ABC e
24	675.5	17.7	604	2	F69802	ABC transporter (A
25	673.5	17.6	600	2	H98149	ATP-binding transp
26	673.5	17.6	600	2	AD3138	hypothetical prote
27	671.5	17.6	611	2	AH3540	ABC transporter AT
28	671.5	17.6	863	2	C90482	ABC transporter, A
29	670.5	17.6	546	2	AG1886	ATP-binding protei
30	670.5	17.6	707	1	LEECB	hemolysin secretio
31	669.5	17.5	707	2	S10057	ABC-type transport
32	668.5	17.5	584	2	E83767	ABC transporter (A
33	665.5	17.4	599	2	AD3017	hypothetical prote
34	665.5	17.4	599	2	D98267	ABC transporter AT
35	665	17.4	600	2	AI2454	ATP-binding protei
36	662	17.3	650	2	T17482	ABC-type transport
37	659	17.3	595	2	T31077	probable ABC-trans
38	655	17.2	582	2	AF0614	probable transport
39	653	17.1	607	2	A95911	hypothetical prote
40	653	17.1	708	2	C30169	leukotoxin express
41	652	17.1	582	2	E90753	ATP-binding transp
42	652	17.1	582	2	S27998	probable ABC-type
43	652	17.1	582	2	C85617	ATP-binding transp
44	651	17.1	893	2	AH2007	toxin secretion AB
45	649.5	17.0	707	2	A61378	leukotoxin express

ALIGNMENTS

RESULT 1

T10657

probable ABC-type transport protein T5F17.80 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-Oct-2004

C;Accession: T10657

R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Banc submitted to the Protein Sequence Database, June 1999

A;Reference number: Z16533

A;Accession: T10657

A;Molecule type: DNA

A;Residues: 1-677

A;Cross-references: UNIPROT:Q9M0G8; UNIPARC:UPI00000A7E39; EMBL:AL049917; GSPDB:GN0006

A;Experimental source: cultivar Columbia; BAC clone T5F17

C;Genetics:

A;Gene: ATSP:T5F17.80

A;Map position: 4

A;Introns: 519/3

F;452-646/Domain: ATP-binding cassette homology

SCORE Search Results Details for Application 10762596 and Search Result us-10-762-596-4.rup.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10762596 and Search Result us-10-762-596-4.rup.

start

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OM protein - protein search, using sw model

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Run on:      July 25, 2006, 21:30:09 ; Search time 186.5 Seconds
              (without alignments)
              3705.022 Million cell updates/sec
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Title:          US-10-762-596-4
Perfect score: 3816
Sequence:      1 MHSWRWAAAAAAFEKRRHSA.....RKKLQEEIVNSVKGCGNCSC 747
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

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Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
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                  Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
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1	3809	99.8	752	1	ABCB7_HUMAN	O75027 homo sapien
2	3519	92.2	752	1	ABCB7_RAT	Q704e8 rattus norv
3	3508	91.9	752	2	Q3U7S8_MOUSE	Q3u7s8 m bone marr
4	3336	87.4	694	1	ABCB7_MOUSE	Q61102 mus musculu

5	3193.5	83.7	651	2	Q2PFV1_MACFA	Q2pfv1 macaca fasc
6	2570	67.3	644	2	Q4SJU8_TETNG	Q4sju8 tetraodon n
7	1894.5	49.6	594	2	Q7Q5L7_ANOGA	Q7q5l7 anopheles g
8	1876	49.2	743	2	Q9W0C5_DROME	Q9w0c5 drosophila
9	1859.5	48.7	709	2	Q7KVB1_DROME	Q7kvb1 drosophila
10	1846	48.4	606	2	Q7KVA9_DROME	Q7kva9 drosophila
11	1800	47.2	703	2	Q71JP9_CAEEL	Q71jp9 caenorhabdi
12	1794	47.0	715	2	Q61XG8_CAEER	Q61xg8 caenorhabdi
13	1716	45.0	728	2	Q9LVM1_ARATH	Q9lvm1 arabidopsis
14	1704	44.7	728	2	Q9LF78_ARATH	Q9lf78 arabidopsis
15	1685	44.2	733	2	Q658I3_ORYSA	Q658i3 oryza sativ
16	1651.5	43.3	677	2	Q9M0G8_ARATH	Q9m0g8 arabidopsis
17	1651.5	43.3	678	2	Q9FUT3_ARATH	Q9fut3 arabidopsis
18	1626	42.6	727	2	Q4WLN7_ASPFU	Q4wln7 aspergillus
19	1616	42.3	716	2	Q7RX59_NEUCR	Q7rx59 neurospora
20	1614.5	42.3	680	2	Q9M0G9_ARATH	Q9m0g9 arabidopsis
21	1614	42.3	698	2	Q4HVV7_GIBZE	Q4hvu7 gibberella
22	1612	42.2	720	2	Q2ULH4_ASPOR	Q2ulh4 aspergillus
23	1596	41.8	763	2	Q4PH16_USTMA	Q4ph16 ustilago ma
24	1594	41.8	697	2	Q8T9W2_DICDI	Q8t9w2 dictyosteli
25	1551.5	40.7	734	2	Q5KBN9_CRYNE	Q5kbn9 cryptococcu
26	1551	40.6	701	2	Q5B1Q2_EMENI	Q5blq2 aspergillus
27	1550.5	40.6	734	2	Q55NA7_CRYNE	Q55na7 cryptococcu
28	1549.5	40.6	696	2	Q6BXD7_DEBHA	Q6bxd7 debaryomyce
29	1538.5	40.3	693	1	YD01_SCHPO	O14286 schizosacch
30	1517.5	39.8	690	1	ATM1_YEAST	P40416 saccharomyc
31	1516.5	39.7	720	2	Q6CX96_KLULA	Q6cx96 kluyveromyc
32	1504	39.4	691	2	Q751N2_ASHGO	Q751n2 ashbya goss
33	1501.5	39.3	750	2	Q59R09_CANAL	Q59r09 candida alb
34	1496	39.2	727	2	Q6FIK3_CANGA	Q6fik3 candida gla
35	1466	38.4	605	2	Q7VZK3_BORPE	Q7vzk3 bordetella
36	1455.5	38.1	588	2	Q7WHV3_BORBR	Q7whv3 bordetella
37	1454	38.1	710	2	Q6C6N0_YARLI	Q6c6n0 yarrowia li
38	1453.5	38.1	606	2	Q2YB82_NITMU	Q2yb82 nitrospir
39	1452	38.1	605	2	Q7W9X4_BORPA	Q7w9x4 bordetella
40	1451.5	38.0	631	2	Q8ZDI0_YERPE	Q8zdi0 yersinia pe
41	1450.5	38.0	596	2	Q8D129_YERPE	Q8d129 yersinia pe
42	1450.5	38.0	596	2	Q66DG4_YERPS	Q66dg4 yersinia ps
43	1444	37.8	592	2	Q68XG3_RICTY	Q68xg3 rickettsia
44	1443	37.8	600	2	Q4UKL9_RICFE	Q4ukl9 rickettsia
45	1443	37.8	609	2	Q9ZDW0_RICPR	Q9zdw0 rickettsia

ALIGNMENTS

RESULT 1

ABCB7_HUMAN

ID ABCB7_HUMAN STANDARD; PRT; 752 AA.

AC O75027; O75345; Q5VWY7; Q5VWY8; Q9BRE1; Q9UND1; Q9UP01;

DT 15-DEC-1998, integrated into UniProtKB/Swiss-Prot.

DT 01-DEC-2000, sequence version 2.

DT 07-MAR-2006, entry version 54.

DE ATP-binding cassette sub-family B member 7, mitochondrial precursor

DE (ATP-binding cassette transporter 7) (ABC transporter 7 protein).

GN Name=ABCB7; Synonyms=ABC7;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;